

Figure 1. (SEQ ID NO: 1)

CCCGGTCGGAGGTTTCAAGGAATGACTAGATGTGGCACTTAGTGCCATGGTCTAGTTGAC	60
AAGGTGATGGTTGGTCAAAAGTTGGACTCGATGATCTCAGAGTTTTTTTCCAGCCTTAAT	120
AATTCTATGAATTCTGTAATTTTATTCTTGATCTTTTGGAGCGAAGTTTGTGGGGATT	180
TTAGTTTGGTTTCCCTGTCACTGTTTTCTTTCCTTGAAACTGACTTTCATTTGCAACATG	240
AGAATTGCTGTATTTGTCAGGTTACAAGTAGTGCAATGGCTGCTTAGAAGTAGTGAGAAA	300
CATTTAGGGAAATACTGGAGTGAAGCAAACACAGTGGTACTGCCAAACTGTAGCTTTGGG	360
ATTTGAGGAGCCACAGAGTTGTATATAAATTTGTTTAATGATATCCTGCCCTGCCTTCC	420
ATTAATTGCTTGTTTTATGAAACCACTCTTTTTTTTTTTTTTTTTTTTGGCTTCTTCA	480
TATCCTGTGGTAATGAGTTAATGCATTTAGAAGCACATGGCAGAACTAGGAGATCTGTGG	540
ATGACAGTGGTACAGGAGCTCTGAATTTTTTAGATAAACTATGAGAGTGGAACAGAAAT	600
CTGAGGCTAGTTTCTTGAGCTGACTGTAAATTTGTGAGAATATTTTCAAGACTACATTA	660
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GGG	723

Figure 2.

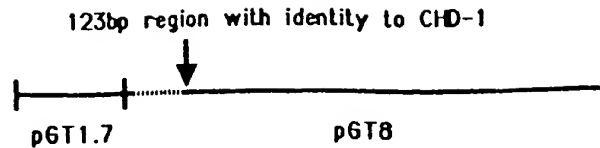


Figure 3.

M CHD-1 ATTCTTCCAG ATGATCCTGA TAAAAACCA CAAGCAAAC AGTTACAGAC (SEQ ID NO: 2)
 C CHD-1A ATTTTACCTG ATGATCCAGA CAAGAAACCC CAGGCAAGC AGCTACAGAC (SEQ ID NO: 3)
 C CHD-W ATTTTACCTG ATGATCCAGA TAAGAAACCC CAGGCTAAGC AGTTACAGAC (SEQ ID NO: 4)
 GT CHD-W ATTTTACCTG ATGACCCAGA TAAGAAACCA CAGGCAAGC AGTTGCAGAC (SEQ ID NO: 5)

M CHD-1 CAAAAACCA CAAGCAAAC AGTTACAGAC CCGTGCAGAC TACCTCATCA
 C CHD-1A CAAGAAACCC CAGGCAAGC AGCTACAGAC CCGTGCAGAC TACCTCATTA
 C CHD-W CAAGAAACCC CAGGCTAAGC AGTTACAGAC CCGTGCAGAT TACCTCATTA
 GT CHD-W CAAGAAACCA CAGGCAAGC AGTTGCAGAC CCGTGCAGAT TACCTCATTA

M CHD-1 AACTACTTAG CAGAGATCTT GCAAAAAGAG AGGCTCAGAG ACTTTGTGGT GCG
 C CHD-1A AATTACTGAA TAAAGACCTT GCAAGAAAGG AAGCACAAG GCTTGCTGGT GCA
 C CHD-W AATTACTGAA TAAAGACCTT GCAAGAAAGG AAGCACAAG ACTTGCTGGT GCA
 GT CHD-W AATTACTGAA TAAAGACCTT GCAAGAAAGG AAGTGCABAAG ACTTACTGGT GCA

M CHD-1 ILPDDPDKKPQAKQLOTRADYLIKLLSRDLAKREAQRLCGA (SEQ ID NO: 6)
 C CHD-1A ILPDDPDKKPQAKQLOTRADYLIKLLNKDLARKEAQRLAGA (SEQ ID NO: 7)
 C CHD-W ILPDDPDKKPQAKQLOTRADYLIKLLNKDLARKEAQRLAGA (SEQ ID NO: 8)
 GT CHD-W ILPDDPDKKPQAKQLOTRADYLIKLLNKDLARKEVQRLTGA (SEQ ID NO: 9)

4090-4100

13

424

Figure 5. (SEQ ID NO: 10)

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1  CGGGCTGCGG CACGAAGCGC ACCGCCGGCG CACGCAGGCT CCGGCCGGGG
51  AAGGCCTGGC CCGCCGAGCC GGACGCACGC AGGTATTTGG GCAAAAATCT
101 TGGCCATCTG TAGAGAATAG CAAGTCAAAC GCATTACTTC GAAAACATAC
151 GGAGTACCAG AAAGGGGATT CTTGACCTAC ACCTTGTAAC CTGAGTGGAC
201 TTTCTTTTAA ACTTCTTAAT ACTTACAATG AATGGGCACA GTGATGAAGA
251 AAGTGTAAGA AACAGCAGTG GAGAGTCAAG CAGATCAGAT GATGATTCTG
301 GGTCACTTTC AGGTTCTGGA TCTGGTTCAA GCTCTGGAAG CAGTAGCGAT
351 GGAAGTAGCA GCCAGTCAGG TAGCAGTGAC TCTGAATCTG GTTCAGAGTC
401 AGGCAGTCAA TCCGAATCAG AGTCTGACAC ATCTAGAGAG AAGAAACAAG
451 TTCAAGCTAA ACCTCCGAAA GCTGACGGAT CTGAGTTTGG GAAGTCCAGT
501 CCAAGCATAC TTGCTGTACA GAGATCAGCA GTGCTCAAGA AGCAACAGCA
551 ACAGCAAAAA GCAGCATCAT CAGACAGTGG TTCAGAAGAG GACTCATCCA
601 GTAGTGAAGA TTCTGCCGAT GATTTCGTCA GTGAACTAA GAAGAAAAAG
651 CATAAAGATG AAGACTGGCA AATGTCAGGG TCAGGGTCAG TATCAGGAAC
701 TGGTTCTGAT TCTGAATCGG CGGAAGATGG GGATAAAAGC AGTTGTGAAG
751 AAAGTGAATC TGACTATGAG CCAAAAAACA AAGTCAAAAG CCGTAAACCT
801 CCAAGCAGAA TTAAGCCAAA AAGTGGGAAA AAGAGCACAG GACAGAAGAA
851 GAGGCAACTT GATTTCATCAG AGGAGGAGGA GGACGATGAT GAAGATTATG
901 ATAAGAGAGG ATCTCGTCGC CAGGCAACAG TGAATGTTAG TTACAAAGAA
951 GCTGAAGAAA CCAAGACAGA TTCTGATGAT TTGCTGGAAG TTTGTGGAGA
1001 GGATGTCCCA CAGACTGAAG AAGATGAATT TGAACTATA GAGAAGTTTA
1051 TGGACAGTCG AATTGGCCGA AAAGGAGCCA CTGGTGCCTC AACCACCATC
1101 TATGCCGTTG AGGCAGATGG TGACCCAAAT GCTGGGTTTG AAAAGTCAAA
1151 GGAGCTGGGA GAAATACAGT ATCTTATTAA ATGGAAAGGC TGGTCACACA
1201 TCCATAACAC TTGGGAAACT GAAGAAACGC TGAAGCAACA AAATGTTAAA
1251 GGAATGAACA AACTGGACAA CTACAAGAAA AAGGATCAGG AGACAAAACG
1301 CTGGCTGAAA AATGCTTCTC CAGAAGATGT GGAATATTAT AACTGCCAGC
1351 AGGAGCTTAC AGATGATCTG CACAAACAAT ATCAAATAGT GGAAAGAATA
1401 ATTGCTCATT CAAATCAAAA GTCAGCAGCT GGTATCCGG ACTACTATTG
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1501 TCATTGCCAA AAAGTTTCAG GCACGCATTG ATGAGTATTT TAGCAGAAAT
1551 CAATCCAAGA CTACTCCCTT TAAGGACTGC AAGGTTCTAA AACAGAGACC
1601 AAGATTTGTT GCACTGAAGA AGCAACCATC TTACATTGGA GGACATGAAA
1651 GTCTGGAGTT AAGAGATTAT CAGTTAAATG GATTGAATTG GCTCGCTCAT
1701 TCATGGTGCA AAGGAAATAG TTGTATTCTT GCAGATGAAA TGGGTCTGGG
1751 TAAACATAA CAAACAATTT CTTTCTGAA CTACCTGTTT CATGAACATC
1801 AACTGTATGG CCTTTTCTT CTGCGCGTGC CACTTCTTAC CTTGACATCT
1851 TGGCAAAGAG AGATTCAAAC TTGGGCTCCT CAGATGAATG CTGTAGTTTA
1901 CTTAGGAGAT ATAAGTAGTA GAAATATGAT AAGGACTCAT GAATGGATGC
1951 ATCCACAGAC TAAACGATTA AAGTTTAAAC TACTTCTGAC GACATATGAA
2001 ATTTTACTGA AGGATAAGTC ATTCCTTGGT GGTCTCAATT GGGCATTCTAT
2051 AGGAGTTGAT GAAGCTCATC GTTTAAAAAA TGATGACTCT CTTCTGTACA
2101 GGACTTTAAT AGACTTTAAG TCCAACCATC GACTTCTGAT TACTGGAACC
2151 CCACTGCAAA ATTCCCTCAA AGAGCTGTGG TCTTTGTTGC ATTTTCATCAT
2201 GCCAGAAAAA TTTTCTCCTT GGAAGATTTT TGAAGAGGAG CATGGCAAAG
2251 GAAGAGAGTA TGGTTATGCA AGTCTTCACA AAGAGCTTGA ACCATTTTTTA
2301 CTAAGAAGAG TTAAGAAAGA TGTAAGAAAG TCTTTACCTG CTAAGGTTGA
2351 ACAAATCTCG AGGATGGAAA TGAGTGCAAT GCAGAAGCAA TATTACAAGT
2401 GGATTTTAAC AAGGAATTAT AAAGCCCTCA GTAAAGGTTT AAAAGGCAGT
2451 ACCTCAGGCT TTCTGAACAT TATGATGAAA CTTAAGAAGT GTTGAACCA
2501 TTGCTACCTC ATTAAGCCAC CAGATGATAA TGAATTTCTAT AATAAACAGG
2551 AGGCCTTACA GCATTTGATA CGTAGCAGCG GGAACTAAT CTTCTTGAC
2601 AAGTACTGA TTCGTCTGCG AGAACGTGGC AACAGAGTTC TGATTTTCTC
2651 TCAGATGGTG AGGATGCTGG ACATCCTAGC AGAATATCTG AAGTATCGCC
2701 AGTTTCCCTT CCAGAGACTT GATGGATCAA TAAAGGGGA ATTGAGGAAG
2751 CAAGCACTGG ATCATTTCOA TGCAGAAGGA TCAGAGGATT TCTGTTTTTT
2801 ACTGTCTACA AGAGCTGGAG GATTAGGTAT TAACTTGGCA TCTGCTGACA
2851 CTGTAGTTAT TTTTGATTCT GACTGGAATC CACAGAATGA TCTGCAGGCA
2901 CAGGCGAGAG CTCATAGAAT TGGACAGAAG AAACAGGTTA ATATTTATCG
2951 GCTAGTCACA AAAGGATCAG TAGAAGAAGA TATTCTTGAA AGAGCCAAGA

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3001 AGAAGATGGT GCTAGACCAT TTAGTAATTC AGAGAATGGA CACGACAGGA
 3051 AAAACTGTTC TGCATACAGG TTCAACTCCA TCAAGCTCTA CACCTTTTAA
 3101 TAAAGAAGAG TTATCAGCTA TTTTGAAAGT TGGTGCTGAG GAACCTCTTA
 3151 AAGAACCTGA AGGAGAAGAA CAGGAGCCCC AGGAAATGGA TATAGATGAA
 3201 ATCTTGAAGA GAGCTGAAAC TCGGAAAAAT GAGCCAGGTC CATTGACTGT
 3251 AGGGGATGAG TTGCTTTCAC AGTTCAAGGT GGCGAACTTT TCCAATATGG
 3301 ATGAAGATGA TATTGAGTTG GAACCAGAAA GAAATTCAAG AAATTGGGAA
 3351 GAAATCATCC CAGAATCCCA ACGGAGAAGG ATAGAGGAGG AGGAAAGACA
 3401 AAAAGAACTT GAAGAAATAT ACATGCTCCC GAGGATGAGA AACTGTGCAA
 3451 AACAGATCAG CTTTAATGGG AGTGAAGGAA GACGCAGTAG GAGCAGAAGA
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 3751 AGGCTTTAAA GGACAATTCA TCTGGACAAG AAAGAGCAGG AGGTAGACTT
 3801 GGGAAAGTTA AAGGCCCAAC GTTTCGAATC TCAGGAGTGC AGGTGAATGC
 3851 AAAACTAGTC ATCTCTCAGC AAGAAGAGCT GGCACCACTG CACAAATCCA
 3901 TTCCTTCAGA TCCAGAAGAA AGGAAAAGAT ATGTCATCCC ATGCCACACC
 3951 AAGGCTGCTC ACTTCGATAT AGATTGGGGT AAAGAAGATG ATTCCAATCT
 4001 GTTAGTAGGC ATCTATGAAT ATGGCTATGG CAGCTGGGAA ATGATAAAAA
 4051 TGGATCCAGA TCTCAGCTTA ACACAGAAGA TTTTACCTGA TGATCCAGAC
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**

4351 TGAATCTGA AAATAAGAA AAATCTAAAA AAATTCATT GCTGGATACT
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 4451 TGAAGAACTC CATCAGAAGA CATTAGTGT GTGCAAGAA AGAATGAGGC
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 4601 TCACATTACA GAATGCCTGA AGGAGTACAC AAATCCCGAG AAAATAAAAC
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 4901 TGATCATCAC AAAGACAGGC ATCAGGGAGA TGCTTACAAG AAAAGTGACT
 4951 CCAGGAAAAG GCCATATTCA GCCTTCAGTA ATGGAAAAGA TCACAGAGAC
 5001 TGGGATCACT ACAAACAGGA CAGCAGATAC TACAGTGATA GTAAACATAG
 5051 AAAGTTAGAT CACCACAGGA GCAGAGACCA CAGGTCAAAC CTGGAAGGAA
 5101 ACTTAAAAGA CAGCCGGGGT CATTCAGATC ACCGCTCCCA TTCAGACCAC
 5151 AGGATACACT CAGATCACCG TTCCACTTCA GAATACAGCC ATCATAAATC
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 5551 ATATTTTGT ATTTAAAGTT TATGCTGCAC TGTGCTGCAA ATGTTGTGGC
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 5651 CTGCCCTTT CAGACTGGAT CTTACTATAA AACTCTTCAT GTCAAAGTGG
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 5851 GTTTACATTG TACACTGCCA CCACCTTGCC GCTTTTCATC ACAAGCTTGA
 5901 ATATTTAAAT TCTGTACCTA CAGTTGTAAG ATAGCCAGGA TTTCTCTGT
 5951 TTGTGATCAG TTATAATGCC TTTTATGAA ACAAAACAA ACACATACCT
 6001 CAATTAATAA AAAAAACACA ACAAACCAA CAAATGGCTG TAAATTATTG
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6601 AAAAAACC

Figure 6.

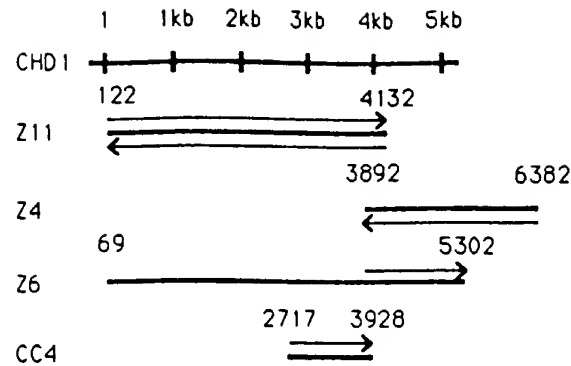


Figure 7.

```

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CHD-W 1 GATGGGATTGTTTCAGTGAACATCCACATAAAAAATAAAAAACAGAAA (SEQ ID NO: 13)
      D G I V S V K H P H K K I K A E (SEQ ID NO: 14)

      K E N E E K P E P D I G I K K E A
CHD-1A 51 AAAGAAAATGAAGAAAAGCCTGAGCCAGATATTGGTATAAAGAAGGAAGCT
CHD-W 51 AAAGAAAATGAAGAAAAGATGAGCCAGAGATTGGTATAAAGAAGGAAGCT
      K E N E E K D E P E I G I K K E A

      E E K R E T K E K E N K R E L K R
CHD-1A 101 GAAAGAAAAAGAGAGACAAAAGAGAAAGAAAATAAAAGGGAATTGAAAAGG
CHD-W 101 GAGAAAAAAGAGAGACAAAAGAAAGGAAAATAAGA
      G E K R E T K E K E N K

      E K K E K E D K K E L K E K D N K
CHD-1A 151 GAGAAAAAGAAAAAGAGGATAAGAAAGAAATTAAGAAAAAGATAATAAA

      E K R E N K V K E S T Q K E K E V
CHD-1A 201 GAAAAGAGAGAAAAACAAAGTAAAGAAATCCACACAGAAAGAAAAAGAAAGTG

      K E E K
CHD-1A 251 AAGGAAGAGAAG

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10
in 137
9307D

Figure 8. (SEQ ID NO: 15)

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ATTTATCGGC TAGTCACAAA AGGATCAGTA GAAGAAGATA TTCTTGAAAG AGCCAAGAAA AAGATGGTGT TAGATCATT
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AGTGATTCAG AGAATGGACA CCACAGGGAA AACTGTACTA CATAACGGCT CTACTCCTTC AAGCTCAACA CCTTTTAATA
  90     100     110     120     130     140     150     160
AGGAAGAGTT ATCAGCAATT TTGAAGTTTG GTGCTGAGGA ACTTTTAAAG GAACCTGAAN NNGAAGAAGA GGAGCCTCAG
  170     180     190     200     210     220     230     240
GAGATGGATA TAGATGAAAT CCTGAAGAGG NCTGAAATC GAGAAAATGA GTCAGGCCCA TTAAGTGTAG GAGATGAGTT
  250     260     270     280     290     300     310     320
ACTTTCACAG TTCAAGGTAG CTAAGTTTTC CAATATGGAT GAAGATGACA TTGAATTGGA ACCAGAACAA AATCTAAGAA
  330     340     350     360     370     380     390     400
ACTGGGAAGA AATCATTCCA GAAGTTCAGT GCGCAGCAAT AGAGGGGNGG GAAAGACAAA AAGAACTTGA AGAAATATAT
  410     420     430     440     450     460     470     480
ATGCTTCCAA GAATGAGAAA CTGTGCAAAA CAGATCAGCT TTAATGGAAA TGAAGGGAGA TGCAGTAGGA GCAGAAGATA
  490     500     510     520     530     540     550     560
TTCTGGATCT GATAGTGATT CCATCTCAGA AAGAAAACGA CCAAAAAAAC GTGGACGACC ACGAACTATT CCCCCTGAAA
  570     580     590     600     610     620     630     640
ACATTAAAGG ATTTAGTGAT GCAGAGATTA GACGATTTAT CAAGAGTTAC AAGAAATTTG GTGGCCCACT TGAAAGGTTA
  650     660     670     680     690     700     710     720
GATGCTATAG CTAGAGATGC TGAGCTAGTT GATAAATCTG AAACAGACCT TAGACGCTCG GGAGAAGTTG TACATAATGG
  730     740     750     760     770     780     790     800
ATGCATTAAAG GCTTTAAATG ATAATGACTT TGGTCAAGGA AGAACAGGTG GTAGATTGGG GAAAGTTAAA GGCCCAACAT
  810     820     830     840     850     860     870     880
TCCGAATAGC AGGAGTGCGAG GTGAATGCAA AGCTAGTCAT TTCTCACGAA GAAGAGTTGG CACCATTGCA TAAATCGATT
  890     900     910     920     930     940     950     960
CCTTCAGATC CAGAAGAAGG GAAAAGATAT GTCATCCCAT ACCACACCAA AGCAGCTCAT TTTGATATAG ATTGGGGTAA
  970     980     990     1000    1010    1020    1030    1040
AGAAGATGAT TCCAATCTGT TAATAGGCAT CTATGAATAT GGTATGGCA GTTGGGAAAT GATAAAATG GATCCTGATC
  1050    1060    1070    1080    1090    1100    1110    1120
TCAGTTTGAC ACAGAAGATT TTACCTGATG ATCCAGATAA GAAACCCAG GCTAAGCAGT TACAGACTCG TGCAGATTAC
  1130    1140    1150    1160    1170    1180    1190    1200
CTCATTAAAT TACTGAATAA AGACCTTCCA AGAAAGGAAG CACAGAGACT TGCTGGTGCA GGCAATTCAA AGAGGAGAAA
  1210    1220    1230    1240    1250    1260    1270    1280
AACAAGAAGT AAGAAGAATA AAGCAACAAA GGCTGC
  1290    1300    1310

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5-

C CHD-1A DARRYLGNLGH*RIASQTHYFENIRSTRKGIILDLHLVT*VDFLNFLLTMNGHSDER (SEQ ID NO: 16)
M CHD-1 PALCPVTVQREPOQETRECRKIFIBILIFEICIHThLLIGDFCFINFLIFTNGHSDER (SEQ ID NO: 17)

C CHD-1A SVRNSGSGESSRSDDDAGSASGSGSGSSGSSSDGSSSQSGSSDSESGSESGSQSESED
M CHD-1 SVRNGSGESSQSGDD-CGSASGSGSGSSGSSSDGSSSQSGSSDSDGSDSGSQSESED
**** * * * * *

C CHD-1A TSREKKQVQAKPKFADGSEFWKSSPSILAVQSAVLKQKQQQ---QKAASSDGSSEEDSS
M CHD-1 TSRENK-VQAKPKFVDGAEPWKSSPSILAVQSAVLKQKQQQPASSNSGSEEDSS
**** * * * * *

C CHD-1A SSEDSDSSSETKKKKKHEDWQMSGSGSVSGTGSDESAEDGDKSSCESESDYEPKN
M CHD-1 SSEDSDSSGAKKKKHEDWQMSGSGSPQLGSDSESEERDKSSCDGTESDYEPKN
**** * * * * *

C CHD-1A KVKSRKPPSRIPKSGKSKSTGQKKQLDSSEEEEDDEDYDKRGSRRQATVNVSYKEAZE
M CHD-1 KVKSRKPPSRIPKSGKSKSTGQKKQLDSSEDEDEDYDKRGSRRQATVNVSYKEDEE
**** * * * * *

C CHD-1A TKTDSDLLLEVCGEDVPQTEDEFETIEKFMDSRIGRKATGASTTIYAVEADGDPNAGF
M CHD-1 MKTDSDLLLEVCGEDVPQTEDEFETIERVMDCRVGRKATGASTTIYAVEADGDPNAGF
**** * * * * *

C CHD-1A KTKXEGEIQYLKWKGNSHIHNTWETEETLAKQNVKGMKLDNYKKKQDETKRWLNAS
M CHD-1 ERKKEGEIQYLKWKGNSHIHNTWETEETLAKQNVKGMKLDNYKKKQDETKRWLNAS
ERKKEGDIQYLKWKGNSHIHNTWETEETLAKQNVKGMKLDNYKKKQDETKRWLNAS
* * * * *

HUMAN PEDVEYNNCOQLTDDLEKQYQIVERTNXSPQSKSAAGYP (SEQ ID NO: 18)
C CHD-1A PEDVEYNNCOQLTDDLEKQYQIVERI IAHSNQKSAAGYPDYCKWGLPYSECSWEDGA
M CHD-1 PEDVEYNNCOQLTDDLEKQYQIVERI IAHSNQKSAAGLPDYCKWGLPYSECSWEDGA

C CHD-1A LIAKKPQARIDEYFSRNQSKTTPFKDCKVLKQRPFRFVALKQPSYIGGHELELRDYQLN
M CHD-1 LISKFPQTCIDEYFSRNQSKTTPFKDCKVLKQRPFRFVALKQPSYIGGHELELRDYQLN
* * * * *

C CHD-1A GLNLWLAESWCKGNSCILADEMGLGKTIQTISFLNYLFHEHQLYGPFLLRVPLSTLTSWOR
M CHD-1 GLNLWLAESWCKGNSCILADEMGLGKTIQTISFLNYLFHEHQLYGPFLLRVPLSTLTSWOR

C CHD-1A EIQTWAPQNAVVLGDIITSRNMI RTHEWHEPQTKRLKFNILLTTYEILKDKSFLGGLN
M CHD-1 EIQTWASQNAVVLGDIITSRNMI RTHEWHEPQTKRLKFNILLTTYEILKDKRFLGGLN

C CHD-1A WAFIGVDEAERLKNDDSLLYRTLIDFKSNERLLITGTPQLNSLKLWLSLLEFIMPEKFPSS
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C CHD-1A WEDFEEZHGKGREYGYASLHKELEPFLLRVVKDVEKSLPAKVEQILRMEMSALQKQYYK
M CHD-1 WEDFEEZHGKGREYGYASLHKELEPFLLRVVKDVEKSLPAKVEQILRMEMSALQKQYYK

C CHD-1A WILTRYKALS KSGSGTSGFLNIMELKCCCNHCYLIKPPDDNEFYNKQALQHLIRSS
M CHD-1 WILTRYKALS KSGSGTSGFLNIMELKCCCNHCYLIKPPDDNEFYNKQALQHLIRSS

C CHD-1A GKLILDKLLIRLRERGNRVLIFSQHVRLMILAEYLYKQRPFPQRLDGSIGKELRKQAL
M CHD-1 GKLILDKLLIRLRERGNRVLIFSQHVRLMILAEYLYKQRPFPQRLDGSIGKELRKQAL

C CHD-1A
M CHD-1

DEFNAGSEDFCFLSTRAGGLGINLASADTVVIFDSWNPQNDLQAQARAERIGQKKQV
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C CHD-W
C CHD-1A
M CHD-1

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C CHD-W
C CHD-1A
M CHD-1

ILKFGAEELFKPEPEXEEEPQEMDIDEILKRAETRENEGGLTVGDELLSQFKVANFSNM
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C CHD-W
C CHD-1A
M CHD-1

DEDDIELEPEQNLNWEI IPEVQWRRIEGKERQKELEIYMLPRMNCARDISFNGNEG
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DEDDIELEPERNSRNWEI IPESQRRIEEERQKELEIYMLPRMNCARDISFNGSEG

C CHD-W
C CHD-1A
M CHD-1

RCSRSRRYSGSDSDSISERKRPKRGRPTIPRENIGFSDAEIRRFIKSYKFGGPVER
RRSRRRYSGSDSDSISERKRPKRGRPTIPRENIGFSDAEIRRFIKSYKFGGPLER
RRSRRRYSGSDSDSITERKRPKRGRPTIPRENIGFSDAEIRRFIKSYKFGGPLER

C CHD-W
C CHD-1A
M CHD-1

LDALARDAELVDKSETDLRRLGELVHNGCIKALNDNDFGQGRGGRGKVGKPTFRISGV
LDALARDAELVDKSETDLRRLGELVHNGCVKALKDSGSGTERAGGRGKVGKPTFRISGV
LDALARDAELVDKSETDLRRLGELVHNGCIKALKDNSSQGERAGGRGKVGKPTFRISGV

C CHD-W
C CHD-1A
M CHD-1

QVNAKLVISHEEELAPLHKSIPSDPEERKRYVPIYHTKAAHFDIDWGEDDSNLLIGIYE
QVNAKLVLAEDELIPLEKSIIPSDPEERKQYTIPTCTKAAHFDIDWGEDDSNLLIGIYE
QVNAKLVISHEEELAPLHKSIPSDPEERKRYVPIYHTKAAHFDIDWGEDDSNLLIGIYE

C CHD-W
C CHD-1A
M CHD-1

YGYGSWEMIKMDPDLSTQKILPDOPDKKQAKQLQTRADYLIKLLNKDLARKEAQRLAG
YGYGSWEMIKMDPDLSTQKILPDOPDKKQAKQLQTRADYLIKLLSRDLAKREAZQRLOG
YGYGSWEMIKMDPDLSTQKILPDOPDKKQAKQLQTRADYLIKLLNKDLARKEAQRLAG

C CHD-W
C CHD-1A
M CHD-1

AGNSKRKRKTRSKKATKAA
AGGSKRKRKTRAKSKAMKSIVKEEIKSDSSPLPSEKSEDDDD----KLNDKSPESKDRS
AGNSKRKRKTRANKK--MKASKIKEEIKSDSSPOPSEKSEDDDEEDNKVNEKSKNKKS

C CHD-1A
M CHD-1

KKSVSDAPVHITASGEFVPIAESEZELDQKTFICKERMRPVKAALKQLDRPEKGLSER
KKIPLDTPVHITATSEFVPISESEZELHQKTFVCKERMRPVKAALKQLDRPEKGLSER

C CHD-1A
M CHD-1

EQLHTRQCLIKIGDHITECLKEYSNPEQIKQWRKNLWIFVSKTFEDARKLHLYKHAI
EQLHTRQCLIKIGDHITECLKEYTNPEQIKQWRKNLWIFVSKTFEDARKLHLYKHAI

C CHD-1A
M CHD-1

KKQESQQNSDQN-SNVATTVIRNPDMEIRKENTNEDDSSRDSYSSDRHLSQYHDEHKD
KKQESQQHNDQNISSNVTVIRNPDVERLKETTNEDDSSRDSYSSDRHLSQYHDEHKD

C CHD-1A
M CHD-1

REQGDSYKKSRSRKPYSFSGKDHREWDHYRQDSRYYSREKXKLLDDEHRSREHRPSL
REQGDAYKKSRSRKPYSFSGKDHREWDHYRQDSRYYSDS--KXKLLDDEHRSRDEHNSL

C CHD-1A
M CHD-1

EGGLKD-CHSDHRSBDSHMEBDSHSTPSTHIIINPRDYRLSDWQDHERAASSGPRSP
EGNLKDSRGHSDHRSBDSHMEBDSHSTSEYSHKSSRDYRHSWQDHERASGSGPRSP

C CHD-1A
M CHD-1

LDQRSYPYGRSP-----FEHSAHERSTPEHTWSSRKTQKLMSSSGTLFXP
LDQRSYPYGRSPGLHRSPPFEHSSDEKSTPEHTWSSRKTQRLTFSGPSFXPYTVNXBSNC

C CHD-1A
C CHD-1A
C CHD-1A
C CHD-1A
C CHD-1A
C CHD-1A
C CHD-1A

LTXLERYGLDILSVAVLLLSRMQGLLSQKKNIIVYKVIAALCKCCGTTFLNRCGLL
LQGPQHCPPQTGSYYKTLFVKVVLGXTQIKLCLXMTXLTLCAYSGKNGGFIIFYFLVE
NSQGLCSLSKATCLBCTLRPPCRFSSQAXIFKCTYSCKLARI SPVCDQLCLFMKQTNK
QKTIKKNTTKPTNGCKLLXINXMSFFPSGFFWLFLSPTTQAFPSQSYTYHFXNISME
SECKNGEKNILFLVLFLFYWILLBTCFWLFTYFFFYXTVSVVIVVNSENIPLXTVPWK
AFQVWFKRRKCSIGEBFKTQISQDSLXIHFLSLFMGNNVKCAMQQLIFKXIXMTLLTE
LLQCTLIVHRXLLSDKLNKPKPT

Figure 10.

55	KPPKADGSEFWKSSPSILAVQRSVAVLKQOQQQKQSSSSE	104 (SEQ ID NO: 20)
2654	MAAKDISTEVLQN.PELYGLRRS...HRAAAHQNYFNDSDDDD...E	2695 (SEQ ID NO: 21)
105	DSADSSSETKKKKHKDEDWQMSGSGSVSGTGSDESAEDGKSSCEESE	154
2696	DNIKQSRKRMTTIEDDED.....EFEDEEGEEDSGEDEDEEDFEEDD	2738
155	SDYEPKNKVKSRKPPSRIPKPSGKSTGQKKRQLDSSEEEEDDEDYDKR	204
2739	DYYGSPKQNRSKPKSRTKSKSKPKSQSEKQSTVKIP.....TRF	2780
205	GSRRQATVNVSYKEAEETKTDSDDLLE...VCGEDVPQT...EDEFE	246
2781	SNRQNKTVNYNIDYSDDDLLESEDDYGSEEALEENVEASANPQPEDFH	2830
247	TIEKFMSRIGRKATGASTTIYAVEADGDPNAGFEKSKELGEIQYLIKW	296
2831	GIDIVINRL.....KTSLEEGKVLEKTVPLNNCKE..NYEFLIKW	2870
297	KGWSHIENWTETEETLKQONVKGMNKLDNYKKK...DQETKRWLKNASPE	343
2871	TDESHLNTWETYESIGQ..VRGLKRLDNYCKQFIIEDQQVRLDPYVTAE	2918
344	DVEYYNCQOELTDDLHKQYQIVERIIA..HSNQKSAAGYPDYCKWQGLP	391
2919	DIEIMDMERERRLDEFEEFHVPERIIDSQRASLEDGTSQQLYLVKWRRLN	2968
392	YSECSWEDGALIAKKFQARIDEYFSRNQSKTTPFKDCKVLKQRPFRVALK	441
2969	YDEATWENATDIVKLAPEQVKHFPQNRNSKILPQYSSNYTSQRPFEKLS	3018
442	KOPSYIGGHESLELRDYQLNGLNWLASHSWCKGNSCILADEMGLKGTIQT	491
3019	VQPPFIKGG...ELRDPQLTGINWMAFLWSKGDNGILADEMGLKGTVQTV	3065
492	SFLNYLFHEHQLYGPFLLRVPLSTLTSWQREIQTWAPQMNNAVYVYLGDIS	541
3066	AFISWLIFARRQNGPHIIVVPLSTMPAWLDTFEKWAPDLNCICYMGNQKS	3115
542	RNMIRTHEW...MHPQTKRLKFNILLTTYEILLKDKSFLGGLNWFAGIV	587
3116	RDITREYEFYTNPRAGKTKMKNVLLTTYEYILKDRALGSIKWQFMAV	3165
588	DEAHLKNDSDLLYRTLIDFKSNHRLITGTPLQNSLKLWSLLHFMPE	637
3166	DEAHLKNAESSLYESLNSPKVANRMLITGTPLQNNIKELAAALVNFLMPG	3215
638	KFSSWEDFE.EEHGKGREYGYASLHKELEPFLLRVKKDVEKSLPAKVEQ	686
3216	RFTIDQEI DFENQDEEQEYIHDLHRRIQPFILRLKKDVEKSLPSKTER	3265
687	ILRMEMSALQKQYKWLTRNYKALSKSGKSTSGFLNIMMELKKCCNHC	736
3266	ILRVELSDVQTEYKYNILTKNYSALTAGAKGGHFSLLNIMNELKKASNEP	3315
737	YLIKPPDDNEF.....YNKQEALQHLIRSSGKLILLDKLLIRLRERGN	779
3316	YLPDAEERVLQKFGDGKMTRENVRLGLIMSSGKMVLDDQLLTRLKKDGB	3365

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780 RVLIFSOMVRMLDILAELKYRQFFQRLDGSIKGELRKQALDBFNAEGS 829
3366 RVLIFSOMVRMLDILGDYLSIKGINFQRLDGTVPQAQRISIDHFNPSDS 3415
830 EDFCFLSTRAGGLGINLASADTVVIFSDWNPNQDLQAQARAHRIGQKK 879
3416 NDFVFLSTRAGGLGINLMTADTVVIFSDWNPNQDLQAQARAHRIGQKN 3465
880 QVNIYRLVTKGSVEEDILERAKKMMVLDELVIQRMDDTGKTVLHTGSTPS 929
3466 HVMVYRLVSKDTVEEVLERARKKMLEYAIISLGVTDGKNKYTKKNP... 3513
930 SSTPFNKEELSAILKFGAEELFKEPEGEQEPQEMDIDEILKRAETRENE 979
3514NAGELSAILKFGAGNMFTATD.NQKKLEDNLDDVLNHAEDHVT 3557
980 PG...PLTVGDELLSQFKVANFSNMDEDDIELEPERNSRNWEEIIPESQR 1026
3558 PDLGESHGGEFLKQFEVTDY.....KADIDWDDIPEEEL 3594
1027 RRIEEERQKELEE.....IYMLPRMRNCAQI..SFNGSE..... 1060
3595 KKLQDEEQKRKDEEYVKEQLEMMNRDNALKKIKNSVNGDGTANSDD 3644
1061 ..GRSRSSRYSGSDSITERKRPKKGRPTIPR.ENIKGFS...AE 1104
3645 DSTSRSSRRRARANDMSIGE...SEVRALYKAILKFGNLKEILDELIAD 3691
1105 IRRFIKSYKKFGGPLERLDAVARDA.....ELVDKSETDLRRLGEL 1145
3692 GTLPVKSPFEKYGETYDEMMEAAKDCVHEEKNRKEILEKLEKHATAYRAK 3741
1146 VHNGCIKALKD.NSSQERAGGRGLKVGKPTFRISGVQ.VNAKLVISHEE 1193
3742 LKSGEIKAEQPKDNPLTRLRLKREKKAVLNFNGVKSLNAESLLSRVE 3791
1194 ELAPLEKSIPSD.PEERKRYVIPCHTKAA..HFDIDWGKEDDSNLLVGIY 1240
3792 DLKYLKNLINSNYKDDPLKPSLGNNTPKPVQNWSSNWTKEEDEKLLIGVF 3841
1241 EYGYGSWEMIKMDPDLSTQKILPDD..... 1266
3842 KYGYGSWTQIRDDPFLGITDKIFLNEVHNPVAKKSASSDTPTPSKKGK 3891
1267PDKKPOAKQLQTRADYLIKLLNKDLARK.....EAQRLAGAGNS 1305
3892 GITGSSKKVFGAHLGRVDYLLSFLRGGLNTKSPSADIGSKKLPTGPSK 3941
1306 KRRKTRNKKNMKASKIKEIKSDSSPQSEKSDDEE...EDNKVNEM 1352
3942 KRQRKPANHSKSMTPETSSPANGPPSKRMKALPKGPAALINWTRLSN 3991
1353 KSENKEKSKIPLLDTPVHITATSEPVPISESEELHQKTFVCKERM RP 1402
3992 SPTPPLKSKVSRDNGTR....QSSNPSSGSAHEKEYDSMDEEDCRHTMSA 4037
1403 VKAALKQLDRPEKGLSEREQLEHTRQCLIKIGDHITECLKEYTNPEIQ 1452
4038 IRTSLKRLRRGGKSLDRKEWAKILKTELTTIGNBI.ESQKGSSRKASPEK 4086
1453 WRKNLWIFVSKF..TEFDARKLEKLYKBAIKKROESQ 1488
4087 YRKELWSYSANFWPADVKSTKLAMY....DKITESQK 4120

Figure 11.

CCHD	AVEAD	GDPNAGFEKSKELGE.IQYLIKWKGWSHIBNTWETEET	LKQONVRGMNKLDNYKK (SEQ ID NO: 22)
MCHD	AVEAD	GDPNAGFERNKEPGD.IQYLIKWKGWSHIBNTWETEET	LKQONVRGNKKLDNYKK (SEQ ID NO: 23)
YCHD	EGKVL	EKTVPDLNCKE..N.YEFLIKWTDESHIBNTWETYES	IGQ..VRGLKRLDNYCK (SEQ ID NO: 24)
		****	****
DHP1	EEEE	YAVEKIIDRRVRKKG.VEYLLKWKGYPETENTWEPENN	LDCQDLIQY (SEQ ID NO: 25)
BHP1	EDEE	YVVEKVLDRRVKKGQVEYLLKWKGFSSEBNTWEPEKN	LDCPELISEF (SEQ ID NO: 26)
MMOD1	EEEE	YVVEKVLDRRVKKG.VEYLLKWKGFSDEDNTWEPEEN	LDCPDLIAEF (SEQ ID NO: 27)
MMOD2	AEPE	FVVEKVLDRRVVNGK.VEYFLKWKGFTDADNTWEPEEN	LDCPELIEDF (SEQ ID NO: 28)
	**	****	****
DPC	PVDLV	YAAEKIIQKRVKGV.VEYRVKWKGNQRYNTWEPENN	ILDRRLIDY (SEQ ID NO: 29)
MMOD3	VGEQV	FAAECILSKRLRKGK.LEYLVKWRGWSSKHSWEPEEN	ILDPRLLLAF (SEQ ID NO: 30)
	*	****	****
		****	****

Figure 14.

MOUSE	CHD1	AGA TAT TCT GGA TCT GAT AGT GAT TCA ATC TCG GAA	(SEQ ID NO: 31)
CHICKEN	CHD-1A	--- --- --- --- --- --- --- ---C ---C --- A-A ---	(SEQ ID NO: 32)
SPIX	CHD-1A	--- --- --- --- --- --- --- ---C ---C --- --- ---	(SEQ ID NO: 33)
CHICKEN	CHD-W	--- --- --- --- --- --- --- ---C ---C ---A ---	(SEQ ID NO: 34)
SPIX	CHD-W	--- --- --- --- --- --- --- ---C ---C ---A ---	(SEQ ID NO: 35)
HYACINTH	CHD-W	--- --- --- --- --- --- --- ---C ---C ---A ---	(SEQ ID NO: 36)
P1		A TAT TCT GGA TCT GAT AGT GAY TC	(SEQ ID NO: 37)
P3		AGA TAT TCC GGA TCT GAT AGT GA	(SEQ ID NO: 38)
MOUSE	CHD1	AGG AAA <u>CGG CCG</u> AAG AAA CGT GGG CGA CCC CGC ACT	
CHICKEN	CHD-1A	--A --- ---A --A --G --- --A A-- --T --A --C	
SPIX	CHD-1A	--- --- ---A --A --G --- --A A-- --A --A ---	
CHICKEN	CHD-W	--A --- --A --A --A --- --A --- --A --A ---	
SPIX	CHD-W	--A --- --A --A -GA --- --A --- --A --A ---	
HYACINTH	CHD-W	--A --- --A --A -GA --- --A --- --A --A ---	
MOUSE	CHD1	ATC CCT CGG GAG AAT ATT AAA GGA TTT AGT GAT GCG GAG	
CHICKEN	CHD-1A	--T --- --A --A --- --- --- --- --- --A ---	
SPIX	CHD-1A	--T --- --A --A --- --A --- --- --- --- --A ---	
CHICKEN	CHD-W	--T --C --T --A --C --- --- --- --- --- --A ---	
SPIX	CHD-W	--T --- --T --A --- --- --- --- --- --- --A ---	
P2		TTT CCT AAA TCG CTA CGT CT	(SEQ ID NO: 39)
HYACINTH	CHD-W	--- --- --- --- --- --- --- --C --- --A --G	
HYACINTH	CHD-W	ATT AGG CGG T	